

Related Structures

Sequences producing significant alignments:			Score (bits)	E Value
gi 7019846 dbj BAA90893.1 	unnamed protein product [Homo sa...	677	0.0	
gi 31542986 ref NP_060095.2 	intelectin; endothelial lectin...	674	0.0	
gi 37724005 gb AAO17800.1 	intelectin [Homo sapiens]	672	0.0	
gi 18254480 ref NP_543154.1 	intelectin 2; endothelial lect...	562	e-159	
gi 6754388 ref NP_034714.1 	intelectin [Mus musculus] >gi 7...	554	e-156	
gi 28932914 gb AAO60215.1 	intelectin 2 [Mus musculus]	540	e-152	
gi 45360437 ref NP_988929.1 	hypothetical protein MGC76330 ...	438	e-121	
gi 20502359 dbj BAB91359.1 	35 kDa serum lectin [Xenopus la...	428	e-118	
gi 28971732 dbj BAC65329.1 	embryonic epidermal lectin [Xen...	426	e-118	
gi 20502361 dbj BAB91360.1 	lectin type 2 [Xenopus laevis]	419	e-116	
gi 49255965 gb AAH71079.1 	Unknown (protein for MGC:79927) ...	408	e-112	
gi 2632076 emb CAA57946.1 	cortical granule lectin [Xenopus...	408	e-112	



gi 1841845 gb AAB47537.1	lectin [Xenopus laevis]	406	e-112	
gi 49115332 gb AAH73311.1	Unknown (protein for MGC:80711) ...	400	e-110	
gi 45360965 ref NP_988850.1	egg cortical granule lectin [X...	399	e-110	
gi 13094239 dbj BAB32787.1	serum lectin [Lethenteron japon...	346	7e-94	
gi 1079283 pir S49589	cortical granule lectin - African cl...	330	5e-89	
gi 11095793 gb AAG30025.1	putative interlectin [Oncorhynch...	117	7e-25	
gi 31196141 ref XP_307018.1	ENSANGP00000016440 [Anopheles ...	48	4e-04	
gi 42524002 ref NP_969382.1	hypothetical protein predicted...	47	6e-04	
gi 42524003 ref NP_969383.1	hypothetical protein predicted...	46	0.001	
gi 120092 sp P19477 FIBA_PARPA	Fibrinogen-like protein A pr...	44	0.007	
gi 34853459 ref XP_342180.1	similar to Rho-guanine nucleot...	44	0.009	
gi 4505065 ref NP_003541.1	MAD1-like 1; MAD1 (mitotic arre...	43	0.016	
gi 47086505 ref NP_997939.1	Unknown (protein for MGC:77116...	42	0.021	
gi 31200947 ref XP_309421.1	ENSANGP00000011252 [Anopheles ...	40	0.10	
gi 41107704 ref XP_031401.4	EGF-like-domain, multiple 3 [H...	39	0.18	
gi 42820328 emb CAF31637.1	keratin associated protein 5-8 ...	39	0.23	
gi 47210774 emb CAF90667.1	unnamed protein product [Tetrao...	39	0.30	
gi 47225870 emb CAF98350.1	unnamed protein product [Tetrao...	39	0.30	
gi 38372386 sp Q9BYQ1 KR95_HUMAN	Keratin associated protein...	39	0.30	
gi 28875408 gb AAO59918.1	fibrinogen related protein 12.1 ...	38	0.39	
gi 28875410 gb AAO59919.1	fibrinogen related protein 12.1-...	38	0.39	
gi 399492 sp P02675 FIBB_HUMAN	Fibrinogen beta chain precur...	38	0.39	
gi 11761631 ref NP_005132.1	fibrinogen, beta chain preprop...	38	0.39	
gi 223002 prf 0401173A	fibrin beta	38	0.39	
gi 182430 gb AAA52429.1	beta-fibrinogen precursor	38	0.39	
gi 2781208 pdb 1FZA B	Chain B, Crystal Structure Of Fibrino...	38	0.39	
gi 24987624 pdb 1LT9 B	Chain B, Crystal Structure Of Recomb...	38	0.39	
gi 49258694 pdb 1RE3 B	Chain B, Crystal Structure Of Fragme...	38	0.39	
gi 47217467 emb CAG10236.1	unnamed protein product [Tetrao...	38	0.51	
gi 47479508 gb AAH69560.1	KRTAP9-2 protein [Homo sapiens]	38	0.51	
gi 46395624 sp O75095 EFL3_HUMAN	Multiple EGF-like-domain p...	38	0.51	
gi 38372389 sp Q9BYQ4 KR92_HUMAN	Keratin associated protein...	38	0.51	
gi 16118240 ref NP_114167.2	keratin associated protein 9.2...	38	0.51	
gi 30409360 dbj BAC76375.1	ficolin-1 [Xenopus laevis]	37	0.67	
gi 34880777 ref XP_222794.2	similar to tenascin-N [Rattus ...	37	0.67	
gi 30409366 dbj BAC76378.1	ficolin-4 [Xenopus laevis]	37	0.87	
gi 30409362 dbj BAC76376.1	ficolin-2 [Xenopus laevis]	37	0.87	
gi 46806224 dbj BAD17448.1	hypothetical protein [Oryza sat...	37	0.87	
gi 28195390 ref NP_689829.2	tripartite motif-containing 42...	37	1.1	
gi 30316326 sp P02678_2	[Segment 2 of 2] Fibrinogen beta c...	37	1.1	
gi 37359684 emb CAE47765.1	SI:bZ1P14.8.1 (novel protein si...	37	1.1	
gi 7441528 pir A25052	fibrinogen beta chain - sea lamprey ...	37	1.1	
gi 21757165 dbj BAC05042.1	unnamed protein product [Homo s...	37	1.1	
gi 23200381 pdb 1LWU B	Chain B, Crystal Structure Of Fragme...	37	1.1	
gi 23104420 ref ZP_00090884.1	COG0500: SAM-dependent methy...	37	1.1	
gi 28195392 ref NP_084495.1	tripartite motif-containing 42...	36	1.5	
gi 27754776 ref NP_003656.2	ficolin 3 isoform 1 precursor;...	36	1.5	
gi 37181268 gb AAQ88448.1	NL3 [Homo sapiens]	36	1.5	
gi 13124185 sp O75636 FCN3_HUMAN	Ficolin 3 precursor (Colla...	36	1.5	
gi 30409364 dbj BAC76377.1	ficolin-3 [Xenopus laevis]	36	1.5	

gi 27754778 ref NP_775628.1	ficolin 3 isoform 2 precursor;...	36	1.5	<input checked="" type="checkbox"/>
gi 34858971 ref XP_215890.2	similar to angiopoietin 3 [Rat...	36	1.9	<input checked="" type="checkbox"/>
gi 9229906 dbj BAB00626.1	fibrinogen-like protein [Ciona i...	36	1.9	<input checked="" type="checkbox"/>
gi 6753006 ref NP_033771.1	angiopoietin 4; angiopoietin 3 ...	36	1.9	<input checked="" type="checkbox"/>
gi 47229454 emb CAF99442.1	unnamed protein product [Tetrao...	36	1.9	<input checked="" type="checkbox"/>
gi 47196977 emb CAF88157.1	unnamed protein product [Tetrao...	36	1.9	<input checked="" type="checkbox"/>
gi 38196089 gb AAR13732.1	fibrinogen [Anopheles gambiae]	35	2.5	<input checked="" type="checkbox"/>
gi 31200995 ref XP_309445.1	ENSANGP00000011248 [Anopheles ...	35	2.5	<input checked="" type="checkbox"/>
gi 9280285 dbj BAB01686.1	unnamed protein product [Macaca ...	35	2.5	<input checked="" type="checkbox"/>
gi 46204657 ref ZP_00049663.2	COG0601: ABC-type dipeptide/...	35	2.5	<input checked="" type="checkbox"/>
gi 31199197 ref XP_308546.1	ENSANGP00000015891 [Anopheles ...	35	2.5	<input checked="" type="checkbox"/>
gi 47228399 emb CAG05219.1	unnamed protein product [Tetrao...	35	2.5	<input checked="" type="checkbox"/>
gi 47522525 dbj BAD20197.1	keratin associated protein [Hom...	35	2.5	<input checked="" type="checkbox"/>
gi 13676535 dbj BAB41181.1	hypothetical protein [Macaca fa...	35	2.5	<input checked="" type="checkbox"/>
gi 745664 prf 2016385A sea	anemone toxin Bg II	35	3.3	<input checked="" type="checkbox"/>
gi 16078002 ref NP_388818.1	similar to cell wall-binding p...	35	3.3	<input checked="" type="checkbox"/>
gi 31200937 ref XP_309416.1	ENSANGP00000011265 [Anopheles ...	35	3.3	<input checked="" type="checkbox"/>
gi 34879228 ref XP_344545.1	angiopoietin-2 [Rattus norvegi...	35	3.3	<input checked="" type="checkbox"/>
gi 33859809 ref NP_862897.1	fibrinogen, B beta polypeptide...	35	3.3	<input checked="" type="checkbox"/>
gi 45383970 ref NP_990520.1	tenascin Y variant [Gallus gal...	32	3.5	<input checked="" type="checkbox"/>
gi 8569622 pdb 1EI3 B	Chain B, Crystal Structure Of Native ...	35	4.3	<input checked="" type="checkbox"/>
gi 399491 sp Q02020 FIBB_CHICK	Fibrinogen beta chain precur...	35	4.3	<input checked="" type="checkbox"/>
gi 38372384 sp Q9BYP9 KR99_HUMAN	Keratin associated protein...	35	4.3	<input checked="" type="checkbox"/>
gi 40646583 gb AAR88166.1	aslectin AL-1 [Armigeres subalba...	35	4.3	<input checked="" type="checkbox"/>
gi 7479340 pir T34649	hypothetical protein SC1A11.02c SC1A...	35	4.3	<input checked="" type="checkbox"/>
gi 47209640 emb CAF93081.1	unnamed protein product [Tetrao...	35	4.3	<input checked="" type="checkbox"/>
gi 33598935 ref NP_663327.1	scavenger receptor class F, me...	34	5.6	<input checked="" type="checkbox"/>
gi 21685564 dbj BAC02696.1	SREC-5 [Homo sapiens]	34	5.6	<input checked="" type="checkbox"/>
gi 32041310 ref ZP_00138893.1	COG2087: Adenosyl cobinamide...	34	5.6	<input checked="" type="checkbox"/>
gi 42661152 ref XP_375452.1	similar to keratin associated ...	34	5.6	<input checked="" type="checkbox"/>
gi 13928546 dbj BAB47147.1	complement component C6 [Branch...	34	5.6	<input checked="" type="checkbox"/>
gi 33598927 ref NP_663324.1	scavenger receptor class F, me...	34	5.6	<input checked="" type="checkbox"/>
gi 33598933 ref NP_663326.1	scavenger receptor class F, me...	34	5.6	<input checked="" type="checkbox"/>
gi 33598931 ref NP_663325.1	scavenger receptor class F, me...	34	5.6	<input checked="" type="checkbox"/>
gi 21685560 dbj BAC02694.1	SREC-3 [Homo sapiens]	34	5.6	<input checked="" type="checkbox"/>
gi 3386666 dbj BAA32041.1	D4 dopamine receptor (D4DR) [Tar...	34	5.6	<input checked="" type="checkbox"/>
gi 33598929 ref NP_003684.2	scavenger receptor class F, me...	34	5.6	<input checked="" type="checkbox"/>
gi 20140022 sp Q14162 SREC_HUMAN	Endothelial cells scavenge...	34	5.6	<input checked="" type="checkbox"/>

Alignments

Get selected sequences	Select all	Deselect all
------------------------	------------	--------------

<input checked="" type="checkbox"/> >gi 7019846 dbj BAA90893.1	<input checked="" type="checkbox"/> unnamed protein product [Homo sapiens]
gi 8096221 dbj BAA96094.1	<input checked="" type="checkbox"/> intelectin [Homo sapiens]
gi 18091783 gb AAL58073.1	<input checked="" type="checkbox"/> endothelial lectin HL-1 [Homo sapiens]
gi 20377087 gb AAM20741.1	<input checked="" type="checkbox"/> intestinal lactoferrin receptor [Homo sapiens]
gi 37181843 gb AAQ88725.1	<input checked="" type="checkbox"/> ITLN [Homo sapiens]

gi|37724012|gb|AA017801.1|  intelectin [Homo sapiens]
gi|44976129|gb|AAS49907.1|  omentin [Homo sapiens]
gi|48146565|emb|CAG33505.1| ITLN1 [Homo sapiens]
 Length = 313

Score = 677 bits (1747), Expect = 0.0
 Identities = 313/313 (100%), Positives = 313/313 (100%)
 Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
 Sbjct: 1 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60




Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY
 Sbjct: 61 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG
 Sbjct: 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 822
 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV
 Sbjct: 181 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS 1002
 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS
 Sbjct: 241 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS 300

Query: 1003 REITEAAVLLFYR 1041
 REITEAAVLLFYR
 Sbjct: 301 REITEAAVLLFYR 313

 >gi|31542986|ref|NP_060095.2|  intelectin; endothelial lectin HL-1; intestinal
 [Homo sapiens]
gi|18088358|gb|AAH20664.1|  Intelectin [Homo sapiens]
 Length = 313

Score = 674 bits (1738), Expect = 0.0
 Identities = 312/313 (99%), Positives = 312/313 (99%)
 Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
 Sbjct: 1 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60



Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKA YPEGDGNWANY
 Sbjct: 61 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKAVYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG
 Sbjct: 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 822
 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV
 Sbjct: 181 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGQREFTAGFVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 1002
 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS
 Sbjct: 241 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 300

Query: 1003 REITEAAVLLFYR 1041
 REITEAAVLLFYR
 Sbjct: 301 REITEAAVLLFYR 313

 >gi|37724005|gb|AA017800.1|  intelectin [Homo sapiens]
 Length = 313

Score = 672 bits (1733), Expect = 0.0
 Identities = 311/312 (99%), Positives = 311/312 (99%)
 Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
 Sbjct: 1 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60





Query: 283 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKA YPEGDGNWANY
 Sbjct: 61 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKAVYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLG 642
 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLG
 Sbjct: 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 822
 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV
 Sbjct: 181 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 1002
 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS
 Sbjct: 241 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYS 300

Query: 1003 REITEAAVLLFY 1038
 REITEAAVLLFY
 Sbjct: 301 REITEAAVLLFY 312

 >gi|18254480|ref|NP_543154.1|  intelectin 2; endothelial lectin HL-2 [Homo sapiens]
 gi|18091785|gb|AAL58074.1|  endothelial lectin HL-2 [Homo sapiens]
 gi|37182928|gb|AAQ89264.1|  ITLN2 [Homo sapiens]
 Length = 325

Score = 562 bits (1449), Expect = e-159
 Identities = 265/319 (83%), Positives = 283/319 (88%), Gaps = 5/319 (1%)
 Frame = +1

Query: 100 TMNQLSFLFLFIATTRGWSTDEANTY---FKEW-TCSSS-PSLPRSCKEIKDECPSAFDG 264
 TM +L FLLF T G S A++ +E+ TC+ S SLPRSCKEIK+ C SA DG
 Sbjct: 7 TMTRLCLFLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERCHSAGDG 66

Query: 265 LYFLRTENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGD 444
 LYFLRT+NGV+YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQG+KADYPEGD

Sbjct: 67 LYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKADYPEGD 126

Query: 445 GNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTG 624
GNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNS+LLRYRT+TG

Sbjct: 127 GNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLRYRTNTG 186

Query: 625 FLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAG 804
FLQ LGHNLFGIYQKYPVKY GKCW DNGP IPVVYDFGDA+KTASYSPYQREF AG






Sbjct: 187 FLQRLGHNLFGIYQKYPVKYRSGKWCNDNGPAIPVVYDFGDAKKTASYSPYQREFVAG 246

Query: 805 FVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTH 984
FVQFRVFNNERAANALCAG++VTGCNTEHHCIGGGG+FP+ P+QCGDFS FDW GYGTH

Sbjct: 247 FVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSAFDWDGYGTH 306

Query: 985 VGYSSSREITEAAVLLFYR 1041
V S SREITEAAVLLFYR

Sbjct: 307 VKSSCSREITEAAVLLFYR 325

>gi|6754388|ref|NP_034714.1|  intellectin [Mus musculus]
gi|7513698|pir|JE0328 intellectin - mouse
gi|3357909|dbj|BAA31992.1|  intellectin [Mus musculus]
gi|12841004|dbj|BAB25043.1|  unnamed protein product [Mus musculus]
gi|37724014|gb|AAO17802.1|  intellectin [Mus musculus]
gi|37724016|gb|AAO17803.1|  intellectin [Mus musculus]
Length = 313

Score = 554 bits (1427), Expect = e-156
Identities = 255/313 (81%), Positives = 278/313 (88%)
Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
M QL FLLF++ TRG S E N W S SLPRSCKEIK E A DGLYFLRT

Sbjct: 1 MTQLGFLLFIMVATRGCSAAEENLDTNRWGNSSFSSSLPRSCKEIKQEHTKAQDGLYFLRT 60

Query: 283 ENGVYIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
+NGVYIYQTFCDMT+ GGGWTLVASVHEN+MRGKCTVGDRWSSQQG++ADYPEGDGNWANY

Sbjct: 61 KNGVYIYQTFCDMTTAGGGWTLVASVHENNMRGKCTVGDRWSSQQGNRADYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
NTFGSAEAATSDDYKNPGY+DIQA++LGIWHVPNKSP+ +WR SSLRYRT TGFLQ LG

Sbjct: 121 NTFGSAEAATSDDYKNPGYFDIQAENLGIWHVPNKSPHLNWRKSSLLRYRTFTGFLQHLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 822
HNLFQ+Y+KYPVKYGEKGCWTDNGP +PVVYDFGDA+KTASYSPY QGREFTAG+VQFRV

Sbjct: 181 HNLFGLYKKYPVKYGEKGCWTDNGPALPVVYDFGDARKTASYSPSPSGQREFTAGYVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS 1002
FNNERAA+ALCAG+RVTGCNTEHHCIGGGG+FP+ P QCGDF+ FDW GYGTH GYSSS

Sbjct: 241 FNNERAASALCAGVRVTGCNTEHHCIGGGGFFPEGNPVQCGDFASFDWDGYGTHNGYSSS 300

Query: 1003 REITEAAVLLFYR 1041
R+ITEAAVLLFYR

Sbjct: 301 RKITEAAVLLFYR 313

>gi|28932914|gb|AAO60215.1| intelectin 2 [Mus musculus]
Length = 313

Score = 540 bits (1391), Expect = e-152
Identities = 249/313 (79%), Positives = 273/313 (87%)
Frame = +1

Query: 103 MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 282
M QL FLLF++ TR S E N W S SLPRSCKEIK E A DGLYFLRT
Sbjct: 1 MTQLGFLFLFIMIATRVCSAAEENLDTNRWGNSSFSSSLPRSCKEIKQEDTKAQDGLYFLRT 60

Query: 283 ENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY 462
ENGVIYQTFCDMT+ GGGWTLVASVHEN++RG+CTVGDRWSSQQG++ADYPEGDGNWANY
Sbjct: 61 ENGVIYQTFCDMTTAGGGWTLVASVHENNLGRCTVGDRWSSQQGNRADYPEGDGNWANY 120

Query: 463 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 642
NTFGSAE ATSDDYKNPGY+DIQA++LGIWHVPN SP+ WRNSSLLRYRT TGFLQ LG
Sbjct: 121 NTFGSAEGATSDDYKNPGYFDIQAENLGIWHVPNNSPHLHTWRNSSLLRYRTFTGFLQRLG 180

Query: 643 HNLFGIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRV 822
HNLFG+YQKYPVKYGEKGCWTDNGP PVVYDFGDAQKTASYSP G+ EFTAG+VQFRV
Sbjct: 181 HNLFGLYQKYPVKYGEKGCWTDNGPAFPVVYDFGDAQKTASYSPSGRNEFTAGYVQFRV 240

Query: 823 FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSS 1002
FNNERAA+ALCAG+RVTCNTEHHCIGGGG+FPE P++CGDF+ FD +GYGTH+ YS+S
Sbjct: 241 FNNERAASALCAGVRVTGCNTEHHCIGGGGFFPEFDPEECGDFAAFDANGYGTHIRYSNS 300

Query: 1003 REITEAAVLLFYR 1041
REITEAAVLLFYR
Sbjct: 301 REITEAAVLLFYR 313

>gi|45360437|ref|NP_988929.1| hypothetical protein MGC76330 [Xenopus tropicalis]
gi|38174756|gb|AAH61445.1| Hypothetical protein MGC76330 [Xenopus tropicalis]
Length = 339

Score = 438 bits (1126), Expect = e-121
Identities = 210/327 (64%), Positives = 238/327 (72%)
Frame = +1

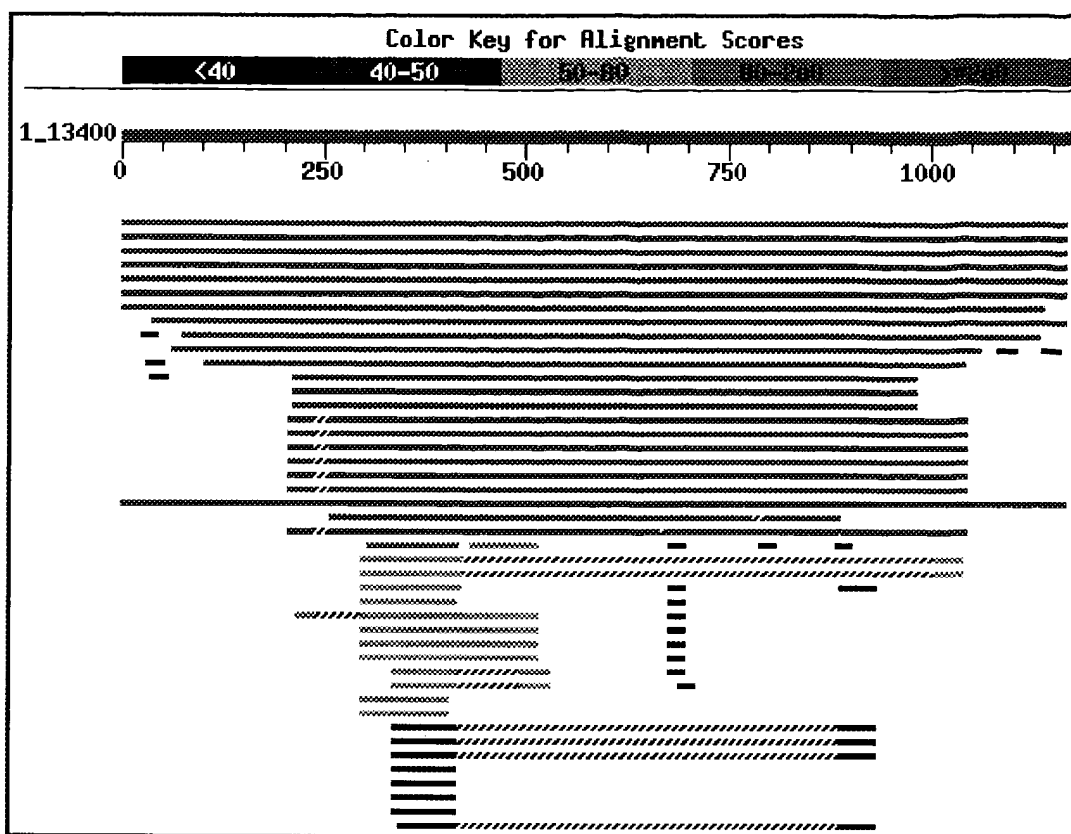
Query: 61 CTQ GKCS*DSDKITMNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKD 240
C Q S +KI L L+A TD + + F RSC EIK
Sbjct: 21 CEQASISEKKEKI-----LNLLACWTEDKTDNSGSRFSGSPTGDMSYGYRSCNEIKS 72

Query: 241 ECPSAFDGLYFLRTENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGS 420
PSA DG+Y L TE+G YQTFCDMT+ GGGWTLVASVHEN+M GKCTVGDRWS+QQG+
Sbjct: 73 SDPSAPDGIYTLATEHGESYQTFCDMTTNGGGWTLVASVHENNMFGKCTVGDRWSTQQGN 132

Query: 421 KADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSL 600
PEGDGNWANY TFG E ATSDDYKNPGYYDIQAK+L +WHVPN +PM +WRNSS+
Sbjct: 133 TLQNPEGDGNWANYATFGLPEGATSDDYKNPGYYDIQAKNLALWHVPNNTPMFNWRNSSI 192

Query: 601 LRYRTDTGFLQTLGHNLFGLIYQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPY 780
LRYRT F G NLF +Y+KYPVKY GKC DNGP +PVVYD G A+KT+S YSP
Sbjct: 193 LRYRTQNSFFTEEGNLFELYKKYPVKYDIGKCLADNGPAVPVVYDLGSAEKTSSLYSPN 252

Query: 781 GQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGF 960
G+ EFTAGFVQFRV N E+AA ALC G++V GCN EHHHCIGGGGYFPE SP+QCGDFS F



Sequences producing significant alignments:

gi 37181842 gb AY358359.1	Homo sapiens clone DNA66308 ITLN...	<u>2317</u>	0.0	LU
gi 37724011 gb AY157362.1	Homo sapiens intelectin (INTL) m...	<u>2317</u>	0.0	LU
gi 44976128 gb AY549722.1	Homo sapiens omentin mRNA, compl...	<u>2307</u>	0.0	LU
gi 18088357 gb BC020664.1	Homo sapiens intelectin 1 (galac...	<u>2292</u>	0.0	LUG
gi 31542985 ref NM_017625.2	Homo sapiens intelectin 1 (gal...	<u>2292</u>	0.0	LUG
gi 37724004 gb AY157361.1	Homo sapiens intelectin (INTL) m...	<u>2286</u>	0.0	LU
gi 18091782 gb AY065972.1	Homo sapiens endothelial lectin ...	<u>2248</u>	0.0	LU
gi 7019845 dbj AK000029.1	Homo sapiens cDNA FLJ20022 fis, ...	<u>2234</u>	0.0	LUG
gi 8096220 dbj AB036706.1	Homo sapiens Itln mRNA for intel...	<u>2095</u>	0.0	LUG
gi 20377086 gb AF271386.1	Homo sapiens intestinal lactofer...	<u>1974</u>	0.0	LU
gi 48146564 emb CR457224.1	Homo sapiens full open reading ...	<u>1855</u>	0.0	
gi 37182927 gb AY358905.1	Homo sapiens clone DNA108701 ITL...	<u>866</u>	0.0	LU
gi 18091784 gb AY065973.1	Homo sapiens endothelial lectin ...	<u>866</u>	0.0	LU
gi 37622351 ref NM_080878.2	Homo sapiens intelectin 2 (ITL...	<u>866</u>	0.0	LU
gi 37724015 gb AY157364.1	Mus musculus intelectin (Intl) m...	<u>676</u>	0.0	LU
gi 12841003 dbj AK007447.1	Mus musculus 10 day old male pa...	<u>676</u>	0.0	LUG
gi 37724013 gb AY157363.1	Mus musculus intelectin (Intl) m...	<u>636</u>	e-179	LU
gi 6754387 ref NM_010584.1	Mus musculus intelectin (Itln),...	<u>636</u>	e-179	LUG
gi 3357908 dbj AB016496.1	Mus musculus mRNA for intelectin...	<u>636</u>	e-179	LUG
gi 28932913 gb AY217760.1	Mus musculus intelectin 2 mRNA, ...	<u>626</u>	e-176	U

gi 22204152 emb AL354714.22	Human DNA sequence from clone ...	551	e-153	
gi 18476709 emb AL591806.16	Human DNA sequence from clone ...	430	e-117	
gi 25046355 gb AC083892.19	Mus musculus chromosome 1 clone...	287	3e-74	
gi 20502360 dbj AB061239.1	Xenopus laevis mRNA for lectin ...	99	1e-17	
gi 41392401 emb BX571811.5	Zebrafish DNA sequence from clo...	73	7e-10	
gi 38564116 emb BX649532.7	Zebrafish DNA sequence from clo...	73	7e-10	
gi 49614137 emb BX284688.12	Zebrafish DNA sequence from cl...	73	7e-10	
gi 49115331 gb BC073311.1	Xenopus laevis cDNA clone MGC:80...	71	3e-09	
gi 49255964 gb BC071079.1	Xenopus laevis cDNA clone MGC:79...	67	5e-08	
gi 2632075 emb X82626.1 XLCORGLEC	X.laevis mRNA for cortica...	67	5e-08	
gi 46040513 dbj BP692558.1	Xenopus laevis NBRP cDNA clone:...	61	3e-06	
gi 1841844 gb U86699.1 XLU86699	Xenopus laevis oocyte lecti...	59	1e-05	
gi 38174755 gb BC061445.1	Xenopus tropicalis hypothetical ...	55	2e-04	
gi 45360436 ref NM_203598.1	Xenopus tropicalis hypotherica...	55	2e-04	
gi 25989471 gb AY079196.1	Xenopus tropicalis egg cortical ...	54	7e-04	
gi 45360964 ref NM_203519.1	Xenopus tropicalis egg cortica...	54	7e-04	
gi 1150691 emb Z50155.1 XLIGF1R	X.laevis mRNA for insulin-l...	52	0.003	
gi 46058673 dbj BP710274.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
gi 46056777 dbj BP708378.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
gi 46038010 dbj BP690055.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
gi 46037729 dbj BP689774.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
gi 28971731 dbj AB105372.1	Xenopus laevis XEEL mRNA for em...	48	0.043	
gi 46083753 dbj BP735160.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
gi 46073306 dbj BP724713.1	Xenopus laevis NBRP cDNA clone:...	48	0.043	
gi 13899443 gb AC026844.4	Homo sapiens chromosome 11, clon...	44	0.67	
gi 31581808 gb AC122375.4	Mus musculus BAC clone RP23-469G...	42	2.6	
gi 15881315 emb AJ336897.1 HSA336897	Homo sapiens genomic s...	42	2.6	
gi 14916182 gb AC092597.1	Homo sapiens BAC clone RP11-100N...	42	2.6	
gi 22266666 dbj AB073013.1	Vitis labrusca x Vitis vinifera...	42	2.6	
gi 22266664 dbj AB073012.1	Vitis labrusca x Vitis vinifera...	42	2.6	
gi 22266660 dbj AB073010.1	Vitis labrusca x Vitis vinifera...	42	2.6	
gi 5442427 gb AF159139.1 AF159139	Gossypium hirsutum phosph...	42	2.6	
gi 47232553 dbj AB111101.1	Vitis vinifera gypsy-type retro...	42	2.6	
gi 47232549 dbj AB111100.1	Vitis vinifera gypsy-type retro...	42	2.6	
gi 47232545 dbj AB097925.1	Vitis vinifera VvmybA3 mRNA for...	42	2.6	
gi 47232543 dbj AB097924.1	Vitis vinifera VvmybA2 mRNA for...	42	2.6	
gi 47232541 dbj AB097923.1	Vitis vinifera VvmybA1 mRNA for...	42	2.6	
gi 22759512 emb AL772367.7	Mouse DNA sequence from clone R...	42	2.6	
gi 49640134 emb CR382121.1	Kluyveromyces lactis strain NRR...	42	2.6	
gi 46090698 dbj BP742105.1	Xenopus laevis NBRP cDNA clone:...	42	2.6	
gi 46088912 dbj BP740319.1	Xenopus laevis NBRP cDNA clone:...	42	2.6	
gi 46084491 dbj BP735898.1	Xenopus laevis NBRP cDNA clone:...	42	2.6	

Alignment(s)

Get selected sequences

Select all

Deselect all

☐ >gi|37181842|gb|AY358359.1| Homo sapiens clone DNA66308 ITLN (UNQ640) mRNA,
Length = 1176

Score = 2317 bits (1169), Expect = 0.0
Identities = 1169/1169 (100%)
Strand = Plus / Plus

```
Query: 1      agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 60
             |||
Sbjct: 1      agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 60

Query: 61      tgtaccaaggaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120
             |||
Sbjct: 61      tgtaccaaggaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120

Query: 121     ctgctgtttctcatagcgaccaccagaggatggagtagagatgaggctaatacttacttc 180
             |||
Sbjct: 121     ctgctgtttctcatagcgaccaccagaggatggagtagagatgaggctaatacttacttc 180

Query: 181     aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac 240
             |||
Sbjct: 181     aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac 240

Query: 241     gaatgtcctagtgcatttgatggcctgtattttctccgactgagaatggtgttatctac 300
             |||
Sbjct: 241     gaatgtcctagtgcatttgatggcctgtattttctccgactgagaatggtgttatctac 300

Query: 301     cagaccttctgtgacatgacctctgggggtggcggtggacctggtggccagcgtgcat 360
             |||
Sbjct: 301     cagaccttctgtgacatgacctctgggggtggcggtggacctggtggccagcgtgcat 360

Query: 361     gagaatgacatgcgtgggaagtgcacggtgggcgatcgctggtccagtcagcagggcagc 420
             |||
Sbjct: 361     gagaatgacatgcgtgggaagtgcacggtgggcgatcgctggtccagtcagcagggcagc 420

Query: 421     aaagcagactaccagagggggacggcaactgggccaactacaacacctttggatctgca 480
             |||
Sbjct: 421     aaagcagactaccagagggggacggcaactgggccaactacaacacctttggatctgca 480

Query: 481     gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 540
             |||
Sbjct: 481     gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 540

Query: 541     ctgggcatctggcacgtgcccaataagtcccccatgcagcactggagaaacagctccctg 600
             |||
Sbjct: 541     ctgggcatctggcacgtgcccaataagtcccccatgcagcactggagaaacagctccctg 600

Query: 601     ctgaggtaccgcacggacactggcttcctccagacactgggacataatctgtttggcatc 660
             |||
Sbjct: 601     ctgaggtaccgcacggacactggcttcctccagacactgggacataatctgtttggcatc 660
```

```

Query: 661  taccagaaatatccagtgaaatatggagaaggaaagtgttggactgacaacggccccgtg 720
          |||
Sbjct: 661  taccagaaatatccagtgaaatatggagaaggaaagtgttggactgacaacggccccgtg 720

Query: 721  atccctgtggtctatgattttggcgacgccagaaaacagcatcttattactcacctat 780
          |||
Sbjct: 721  atccctgtggtctatgattttggcgacgccagaaaacagcatcttattactcacctat 780

Query: 781  ggccagcggaattcactgcggttattgttcagttcaggtatttaataacgagagagca 840
          |||
Sbjct: 781  ggccagcggaattcactgcggttattgttcagttcaggtatttaataacgagagagca 840

Query: 841  gccaacgccttgtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 900
          |||
Sbjct: 841  gccaacgccttgtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 900

Query: 901  ggtggaggaggatactttccagaggccagtcgccagcagtgaggagatttttctggtttt 960
          |||
Sbjct: 901  ggtggaggaggatactttccagaggccagtcgccagcagtgaggagatttttctggtttt 960



Query: 961  gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1020
          |||
Sbjct: 961  gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1020

Query: 1021 gctgtgcttctattctatcggttgagagttttgtgggaggggaacccagacctctcctcca 1080
          |||
Sbjct: 1021 gctgtgcttctattctatcggttgagagttttgtgggaggggaacccagacctctcctcca 1080

Query: 1081 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1140
          |||
Sbjct: 1081 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1140

Query: 1141 gagaaaacaataaatcatattgactcaag 1169
          |||
Sbjct: 1141 gagaaaacaataaatcatattgactcaag 1169

```

 >gi|37724011|gb|AY157362.1|  Homo sapiens intelectin (INTL) mRNA, complete cc
Length = 1203

Score = 2317 bits (1169), Expect = 0.0
Identities = 1169/1169 (100%)
Strand = Plus / Plus

```

Query: 1  agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 60
          |||
Sbjct: 9  agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 68

Query: 61  tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120

```

Sbjct: 69 |||
tgtaccaaggaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 128

Query: 121 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 180
|||

Sbjct: 129 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 188
|||

Query: 181 aaggaatggacctgttcttcgtctccatctctgccagaagctgcaaggaaatcaaagac 240
|||

Sbjct: 189 aaggaatggacctgttcttcgtctccatctctgccagaagctgcaaggaaatcaaagac 248
|||

Query: 241 gaatgtcctagtgcatttgatggcctgtattttctccgactgagaatggtgttatctac 300
|||

Sbjct: 249 gaatgtcctagtgcatttgatggcctgtattttctccgactgagaatggtgttatctac 308
|||

Query: 301 cagaccttctgtgacatgacctctgggggtggcggctggacctggtggccagcgtgcat 360
|||

Sbjct: 309 cagaccttctgtgacatgacctctgggggtggcggctggacctggtggccagcgtgcat 368
|||

Query: 361 gagaatgacatgcgtgggaagtgcacggtgggcgatcgctggtccagtcagcagggcagc 420
|||

Sbjct: 369 gagaatgacatgcgtgggaagtgcacggtgggcgatcgctggtccagtcagcagggcagc 428
|||

Query: 421 aaagcagactaccagagggggacggcaactgggccaactacaacacctttggatctgca 480
|||

Sbjct: 429 aaagcagactaccagagggggacggcaactgggccaactacaacacctttggatctgca 488
|||

Query: 481 gaggcggccacgagcgatgactacaagaacctggctactacgacatccaggccaaggac 540
|||

Sbjct: 489 gaggcggccacgagcgatgactacaagaacctggctactacgacatccaggccaaggac 548
|||

Query: 541 ctgggcatctggcacgtgcccaataagtcccccatgcagcactggagaaacagctccctg 600
|||

Sbjct: 549 ctgggcatctggcacgtgcccaataagtcccccatgcagcactggagaaacagctccctg 608
|||

Query: 601 ctgaggtaccgcacggacactggcttctccagacactgggacataatctgtttggcatc 660
|||

Sbjct: 609 ctgaggtaccgcacggacactggcttctccagacactgggacataatctgtttggcatc 668
|||

Query: 661 taccagaaatatccagtgaatatggagaaggaaagtgttgactgacaacggcccggtg 720
|||

Sbjct: 669 taccagaaatatccagtgaatatggagaaggaaagtgttgactgacaacggcccggtg 728
|||

Query: 721 atccctgtggtctatgattttggcgacgcccagaaaacagcatcttattactcaccctat 780
|||

Sbjct: 729 atccctgtggtctatgattttggcgacgcccagaaaacagcatcttattactcaccctat 788
|||

Query: 781 ggccagcgggaattcactgcgggatttggtcagttcagggtatattaataacgagagagca 840

```
|||||
Sbjct: 789 ggccagcggaattcactgcgggatttgttcagttcagggtatttaataacgagagagca 848

Query: 841 gccaacgccttggtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 900
|||||
Sbjct: 849 gccaacgccttggtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 908



Query: 901 ggtggaggaggatactttccagaggccagtcaccagcagtggtggagatttttctggtttt 960
|||||
Sbjct: 909 ggtggaggaggatactttccagaggccagtcaccagcagtggtggagatttttctggtttt 968

Query: 961 gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1020
|||||
Sbjct: 969 gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1028

Query: 1021 gctgtgcttctattctatcggttgagagttttgtgggaggggaaccagacctctcctcca 1080
|||||
Sbjct: 1029 gctgtgcttctattctatcggttgagagttttgtgggaggggaaccagacctctcctcca 1088

Query: 1081 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1140
|||||
Sbjct: 1089 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1148

Query: 1141 gagaaaacaataaatcatattgactcaag 1169
|||||
Sbjct: 1149 gagaaaacaataaatcatattgactcaag 1177
```

 >gi|44976128|gb|AY549722.1|  Homo sapiens omentin mRNA, complete cds
Length = 1284

Score = 2307 bits (1164), Expect = 0.0

Identities = 1167/1168 (99%)

Strand = Plus / Plus

```
Query: 1 agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 60
|||||
Sbjct: 104 agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 163

Query: 61 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120
|||||
Sbjct: 164 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 223

Query: 121 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaataacttacttc 180
|||||
Sbjct: 224 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaataacttacttc 283

Query: 181 aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac 240
|||||
```

Sbjct: 284 aaggaatggacctgttcttcgtctccatctctgcccagaagctgcaaggaaatcaaagac 343

Query: 241 gaatgtcctagtgcatTTTgatggcctgtatTTTtctccgactgagaatgggtgttatctac 300
|||||

Sbjct: 344 gaatgtcctagtgcatTTTgatggcctgtatTTTtctccgactgagaatgggtgttatctac 403

Query: 301 cagaccttctgtgacatgacctctgggggtggcggctggacctgggtggccagcgtgcat 360
|||||

Sbjct: 404 cagaccttctgtgacatgacctctgggggtggcggctggacctgggtggccagcgtgcat 463

Query: 361 gagaatgacatgcgtgggaagtgcacggtgggcgatcgctgggtccagtcagcagggcagc 420
|||||

Sbjct: 464 gagaatgacatgcgtgggaagtgcacggtgggcgatcgctgggtccagtcagcagggcagc 523

Query: 421 aaagcagactaccagagggggacggcaactgggccaaactacaacacctTTTggatctgca 480
|||||

Sbjct: 524 aaagcagactaccagagggggacggcaactgggccaaactacaacacctTTTggatctgca 583

Query: 481 gaggcggccacgagcgatgactacaagaacctgggtactacgacatccaggccaaggac 540
|||||

Sbjct: 584 gaggcggccacgagcgatgactacaagaacctgggtactacgacatccaggccaaggac 643

Query: 541 ctgggcacatctggcacgtgcccaataagtcccccacgagcactggagaaacagctccctg 600
|||||

Sbjct: 644 ctgggcacatctggcacgtgcccaataagtcccccacgagcactggagaaacagctccctg 703

Query: 601 ctgaggtaccgcacggacactggcttctctccagacactgggacataatctgTTTggcatc 660
|||||

Sbjct: 704 ctgaggtaccgcacggacactggcttctctccagacactgggacataatctgTTTggcatc 763

Query: 661 taccagaaatatccagtgaaatatggagaaggaaagtgttggactgacaacggcccgggtg 720
|||||

Sbjct: 764 taccagaaatatccagtgaaatatggagaaggaaagtgttggactgacaacggcccgggtg 823

Query: 721 atccctgtggtctatgattTTTggcgacgcccagaaaacagcatcttattactcacctat 780
|||||

Sbjct: 824 atccctgtggtctatgattTTTggcgacgcccagaaaacagcatcttattactcacctat 883

Query: 781 ggccagcgggaattcactgcgggatttgttcagttcagggtattttaataacgagagagca 840
|||||

Sbjct: 884 ggccagcgggaattcactgcgggatttgttcagttcagggtattttaataacgagagagca 943

Query: 841 gccaacgccttgtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 900
|||||

Sbjct: 944 gccaacgccttgtgtgctggaatgagggtcaccggatgtaacactgagcaccactgcatt 1003

Query: 901 ggtggaggaggatactTTTccagaggccagtccccagcagtggtggagattTTTtctggtttt 960
|||||

Sbjct: 1004 ggtggaggaggatactttccagagggccagtcgccagcagtggtggagatttttctggtttt 1063

Query: 961 gattggagtgatgatggaactcatgttggttacagcagcagccgtgagataactgaggca 1020
 |||

Sbjct: 1064 gattggagtgatgatggaactcatgttggttacagcagcagccgtgagataactgaggca 1123

Query: 1021 gctgtgcttctattctatcggttgagagttttgtgggaggggaaccagacctctctccca 1080
 |||

Sbjct: 1124 gctgtgcttctattctatcggttgagagttttgtgggaggggaaccagacctctctccca 1183

Query: 1081 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1140
 |||

Sbjct: 1184 accatgagatcccaaggatggagaacaacttaccagtagctagaatgttaatggcagaa 1243

Query: 1141 gagaaaacaataaatcatattgactcaa 1168
 |||

Sbjct: 1244 gagaaaacaataaatcatattgactcaa 1271

>gi|18088357|gb|BC020664.1| Homo sapiens intelectin 1 (galactofuranose bir
 MGC:22348 IMAGE:4693329), complete cds
 Length = 1209

Score = 2292 bits (1156), Expect = 0.0
 Identities = 1165/1168 (99%)
 Strand = Plus / Plus

Query: 1 agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 60
 |||
 Sbjct: 15 agaaagctgcactctgttgagctccagggcgagtgaggaggaggagtgaggagctctc 74

Query: 61 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 120
 |||
 Sbjct: 75 tgtaccaaggaaagtgcagctgagactcagacaagattacaatgaaccaactcagcttc 134

Query: 121 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 180
 |||
 Sbjct: 135 ctgctgtttctcatagcgaccaccagaggatggagtacagatgaggctaatacttacttc 194

Query: 181 aaggaatggacctgttcttcgtctccatctctgccagaagctgcaaggaaatcaaagac 240
 |||
 Sbjct: 195 aaggaatggacctgttcttcgtctccatctctgccagaagctgcaaggaaatcaaagac 254

Query: 241 gaatgtcctagtgcatgttgatggcctgtattttctccgcactgagaatggtgttatctac 300
 |||
 Sbjct: 255 gaatgtcctagtgcatgttgatggcctgtattttctccgcactgagaatggtgttatctac 314

Query: 301 cagaccttctgtgacatgacctctgggggtggcggtggacctggtggccagcgtgcat 360
 |||

Sbjct: 315 cagaccttctgtgacatgacctctgggggtggcggtggaccctggtggccagcgtgcac 374

Query: 361 gagaatgacatgcgtgggaagtgcacgggtgggcgatcgctggtccagtcagcagggcagc 420
 |||
 Sbjct: 375 gagaatgacatgcgtgggaagtgcacgggtgggcgatcgctggtccagtcagcagggcagc 434

Query: 421 aaagcagactacccagagggggacggcaactgggccaactacaacacctttggatctgca 480
 |||
 Sbjct: 435 aaagcagtctacccagagggggacggcaactgggccaactacaacacctttggatctgca 494

Query: 481 gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 540
 |||
 Sbjct: 495 gaggcggccacgagcgatgactacaagaaccctggctactacgacatccaggccaaggac 554

Query: 541 ctgggcatctggcacgtgccaataagtcccccagcagcactggagaaacagctccctg 600
 |||
 Sbjct: 555 ctgggcatctggcacgtgccaataagtcccccagcagcactggagaaacagctccctg 614

Query: 601 ctgaggtaccgcacggacactggcttctccagacactgggacataatctgtttggcatc 660
 |||
 Sbjct: 615 ctgaggtaccgcacggacactggcttctccagacactgggacataatctgtttggcatc 674

Query: 661 taccagaaatatccagtgaaatatggagaaggaaagtgttggactgacaacggcccgggtg 720
 |||
 Sbjct: 675 taccagaaatatccagtgaaatatggagaaggaaagtgttggactgacaacggcccgggtg 734

Query: 721 atccctgtggtctatgattttggcgacgccagaaaacagcatcttattactcacctat 780
 |||
 Sbjct: 735 atccctgtggtctatgattttggcgacgccagaaaacagcatcttattactcacctat 794

Query: 781 ggccagcgggaattcactgcgggatttggttcagttcagggatattaataacgagagagca 840
 |||
 Sbjct: 795 ggccagcgggaattcactgcgggatttggttcagttcagggatattaataacgagagagca 854

Query: 841 gccaacgccttggtgtgctggaatgagggtcaccggatgtaacactgagcatcactgcatt 900
 |||
 Sbjct: 855 gccaacgccttggtgtgctggaatgagggtcaccggatgtaacactgagcaccactgcatt 914

Query: 901 ggtggaggaggatactttccagaggccagtcgccagcagtggtggagatttttctggtttt 960
 |||
 Sbjct: 915 ggtggaggaggatactttccagaggccagtcgccagcagtggtggagatttttctggtttt 974

Query: 961 gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1020
 |||
 Sbjct: 975 gattggagtggatatggaactcatgttggttacagcagcagccgtgagataactgaggca 1034

Query: 1021 gctgtgcttctattctatcggttgagagttttgtgggagggaaaccagacctctcctccca 1080
 |||